

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25
SEQUENCE LISTING

<110> Bayer Cropscience GmbH

<120> Plants with increased activity of a Class 3 branching enzyme

<130> BCS 03-5005-PCT

<150> EP 03090324.9

<151> 2003-09-30

<160> 6

<170> PatentIn version 3.1

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<212> DNA

<213> Solanum tuberosum

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195 200 205

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Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln Thr
245 250 255

Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr
260 265 270

Trp Lys Glu Gln Gln Lys Lys Asp Pro Ala Ser Asn Leu Pro Ser Tyr
275 280 285

Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly
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305 310 315 320

Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr
325 330 335

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340 345 350

Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile
355 360 365

Pro Asp Ala Asp Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro
370 375 380

Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser
385 390 395 400

Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys
405 410 415

Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys
420 425 430

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Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
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Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
515 520 525

Arg Met Phe Lys Tyr Gly Asp Pro Asp Val Leu His Phe Leu Leu Ser
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545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe
565 570 575

Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala
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Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro
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Asn Val Ile Thr Ile Ala Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys
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Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu
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Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly
690 695 700

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25
Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His
705 710 715 720

Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu
725 730 735

Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro
740 745 750

Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp
755 760 765

Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Asp
770 775 780

Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala
785 790 795 800

Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
805 810 815

Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
820 825 830

Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
835 840 845

Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp
850 855 860

Gln Asn Thr Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
865 870 875 880

Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
885 890 895

Thr Arg Ile Leu Arg Ala
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<212> DNA

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<220>

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260 265 270		
act tgg aaa gag caa caa aaa gag gat ccg gca agc aat ttg cca tcg		865
Thr Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser		
275 280 285		
tat gat gtg gta gat agt gga aaa gaa tat gat att tac aat att ata		913
Tyr Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile		
290 295 300		
ggt gat cct gaa tcg ttt aag aaa ttt cgt atg aaa cag cct cct att		961
Gly Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile		
305 310 315		
gct tac tgg tta gaa act aaa aag gga agg aaa ggc tgg tta cag aaa		1009
Ala Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys		
320 325 330 335		
tat atg cct gct tta cct cat gga agc aaa tac agg gtg tat ttt aac		1057
Tyr Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn		
340 345 350		
aca cca aat ggg cct ctt gaa cga gtt cct gcg tgg gcc aat ttt gtc		1105
Thr Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val		
355 360 365		
att cca gat gca ggc ggg atg gca tta gca gtc cat tgg gaa cca cct		1153
Ile Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro		
370 375 380		
cct gaa tat gct tat aaa tgg aaa cac aag cta cca gtc aag cct aag		1201
Pro Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys		
385 390 395		
tcc ttg cgc ata tat gaa tgt cat gtt ggc atc tct ggc cag gaa cca		1249
Ser Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro		
400 405 410 415		
aaa gtt tca tct ttc aat gat ttt att agc aag gtc ctt ccg cat gta		1297
Lys Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val		
420 425 430		
aaa gaa gct gga tac aat gca ata caa att att gga gtt gtt gag cac		1345
Lys Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His		
435 440 445		
aag gat tat ttc act gtt gga tat aga gtg acc aat ttt tat gct gtt		1393
Lys Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val		
450 455 460		
agt agc cgt tat ggc aca ccg gat gac ttc aag cgc ttg gtt gat gaa		1441
Ser Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu		
465 470 475		
gca cat ggg ctt gga ctg ctt gtc ttt ttg gag att gtg cac tct tat		1489
Ala His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr		
480 485 490 495		
gca gca gca gat gaa atg gtt ggg tta tct ctt ttt gat gga gca aat		1537
Ala Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn		
500 505 510		
gat tgc tat ttc cac act ggt aaa cgt gga cac cac aaa ttc tgg ggc		1585
Asp Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly		
515 520 525		

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gcc aac att cac cat gtc aat gat act acc atg gtg att tct tac ttg Ala Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu 800 805 810 815	2449
aga ggt ccc aat ctc ttt gtg ttc aac ttt cat cct gtc aat tca tat Arg Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr 820 825 830 835	2497
gaa aga tac att ata ggt gtg gaa gaa gct gga gag tat caa gtc aca Glu Arg Tyr Ile Ile Gly Val Glu Ala Gly Glu Tyr Gln Val Thr 835 840 845	2545
tta aat aca gat gaa aac aag tat ggt ggt aga gga cta ctt ggc cat Leu Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His 850 855 860	2593
gat cag aat att caa aga acc att agt aga aga gct gat gga atg aga Asp Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg 865 870 875	2641
ttt tgc ttg gaa gtg cct ctg cca agt aga agt gct cag gtc tac aag Phe Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys 880 885 890 895	2689
ttg acc cga att cta aga gca tgatcactct agtaatcaaa gtgcctcata Leu Thr Arg Ile Leu Arg Ala 900	2740
tgatgacaca aaaggaaagg ttctacattg cccttacact gatcaatatt gacacctttc cgaggtgagt ttctgtgatt cttgagcaga ctgtggcta gtcaattatc atgaactttt gccttcagca tccggatagt cgcttctcct gtgcaatgag ggcattggacg aaaaaaaaaa tggcttgtca tgggggtcat aagcatccgc cagattaaga tttcacaggg ctcgagtaaa accatcactt actttaagga tacacaaaca caccaacggg gtgcaggctc tgataccctc taaagtg	2800 2860 2920 2980 3040 3047

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<212> PRT

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<400> 6

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Ser Arg Leu Ser Phe Leu Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln 20 25 30

Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys 35 40 45

Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu 50 55 60

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Lys Tyr Lys Gln Ser Glu Glu Gly Lys Gly Ile Asp Pro Val Gly Phe
65 70 75 80

Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg
85 90 95

Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg
100 105 110

His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met
115 120 125

His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly
130 135 140

Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr
145 150 155 160

Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr
165 170 175

Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Pro Asp
180 185 190

Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Gly Lys Gly
195 200 205

Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu
210 215 220

Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val
225 230 235 240

Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln Thr
245 250 255

Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr
260 265 270

Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser Tyr
275 280 285

Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly
290 295 300

Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile Ala
305 310 315 320

Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr
325 330 335

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn Thr
340 345 350

Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile
355 360 365

Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro
370 375 380

Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser
385 390 395 400

Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys
405 410 415

Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys
420 425 430

Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His Lys
435 440 445

Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser
450 455 460

Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala
465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala
485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
500 505 510

Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
515 520 525

Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu Ser
530 535 540

Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe
545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe
565 570 575

Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala
580 585 590

Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro
595 600 605

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Asn Val Ile Thr Ile Ala Glu Asp Ala Thr Leu Tyr Pro Gly Leu Cys
610 615 620

Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu
625 630 635 640

Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His
645 650 655

Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln
660 665 670

Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile
675 680 685

Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly
690 695 700

Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His
705 710 715 720

Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu
725 730 735

Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro
740 745 750

Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp
755 760 765

Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Gly
770 775 780

Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala
785 790 795 800

Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
805 810 815

Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
820 825 830

Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
835 840 845

Asn Thr Asp Glu Asn Lys Tyr Gly Arg Gly Leu Leu Gly His Asp
850 855 860

Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
865 870 875 880

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
885 890 895

Thr Arg Ile Leu Arg Ala
900